

? ds

Set	Items	Description
S1	39	RUMINANTIUM AND (MAP(W)2 OR MAP2 OR MAJOR(W)ANTIGENIC(W) PR- OTEIN(W)2)
S2	14	RD S1 (unique items)
S3	4334	RUMINANTIUM AND PY<2000
S4	1870	RD S3 (unique items)
S5	410	S4 AND (VACCIN? OR THERAP? OR TREAT?)
S6	265	S4 AND VACCIN?

?

PLEASE ENTER A COMMAND OR BE LOGGED OFF IN 5 MINUTES

?

---Logging off of Dialog---

? logoff

08oct06 15:32:27 User226352 Session D966.5

SYSTEM:OS - DIALOG OneSearch

File 5:Biosis Previews(R) 1969-2006/Oct W1
(c) 2006 The Thomson Corporation

File 6:NTIS 1964-2006/Oct W1
(c) 2006 NTIS, Intl Cpyrght All Rights Res

File 24:CSA Life Sciences Abstracts 1966-2006/Aug
(c) 2006 CSA.

File 34:SciSearch(R) Cited Ref Sci 1990-2006/Oct W1
(c) 2006 The Thomson Corp

File 40:Enviroline(R) 1975-2006/Aug

File 41:Pollution Abstracts 1966-2006/Aug
(c) 2006 CSA.

File 45:EMCare 2006/Oct W1
(c) 2006 Elsevier B.V.

File 50:CAB Abstracts 1972-2006/Sep
(c) 2006 CAB International

File 65:Inside Conferences 1993-2006/Oct 06
(c) 2006 BLDSC all rts. reserv.

File 71:ELSEVIER BIOBASE 1994-2006/Oct W1
(c) 2006 Elsevier B.V.

File 73:EMBASE 1974-2006/Oct 06
(c) 2006 Elsevier B.V.

File 94:JICST-EPlus 1985-2006/Jul W1
(c) 2006 Japan Science and Tech Corp(JST)

File 98:General Sci Abs 1984-2006/Oct
(c) 2006 The HW Wilson Co.

File 103:Energy SciTec 1974-2006/Aug B1
(c) 2006 Contains copyrighted material

*File 103: For access restrictions see Help Restrict.

File 136:BioEngineering Abstracts 1966-2006/Aug
(c) 2006 CSA.

File 143:Biol. & Agric. Index 1983-2006/Jul
(c) 2006 The HW Wilson Co

File 144:Pascal 1973-2006/Sep W2
(c) 2006 INIST/CNRS

File 155:MEDLINE(R) 1950-2006/Oct 09
(c) format only 2006 Dialog

File 156:ToxFile 1965-2006/Oct W1
(c) format only 2006 Dialog

File 162:Global Health 1983-2006/Aug
(c) 2006 CAB International

File 172:EMBASE Alert 2006/Oct 06
(c) 2006 Elsevier B.V.

File 305:Analytical Abstracts 1980-2006/Sep W3
(c) 2006 Royal Soc Chemistry

*File 305: Alert feature enhanced for multiple files, duplicate removal, customized scheduling. See HELP ALERT.

File 369:New Scientist 1994-2006/Aug W2
(c) 2006 Reed Business Information Ltd.

File 370:Science 1996-1999/Jul W3
(c) 1999 AAAS

*File 370: This file is closed (no updates). Use File 47 for more current information.

File 393:Beilstein Abstracts 2006/Q3
(c) 2006 Beilstein GmbH

File 399:CA SEARCH(R) 1967-2006/UD=14515
(c) 2006 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement.

IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec
(c) 2006 The Thomson Corp

\$3.96 0.177 DialUnits File357
 \$3.96 1 Type(s) in Format 7
 \$3.96 1 Types
 \$7.92 Estimated cost File357
 \$12.54 0.534 DialUnits File434
 \$12.54 Estimated cost File434
 OneSearch, 20 files, 9.279 DialUnits FileOS
 \$4.26 TELNET
 \$247.14 Estimated cost this search
 \$252.10 Estimated total session cost 10.144 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 5:Biosis Previews(R) 1969-2006/Oct W1
 (c) 2006 The Thomson Corporation
 File 6:NTIS 1964-2006/Oct W1
 (c) 2006 NTIS, Intl Cpyrght All Rights Res
 File 24:CSA Life Sciences Abstracts 1966-2006/Aug
 (c) 2006 CSA.
 File 34:SciSearch(R) Cited Ref Sci 1990-2006/Oct W1
 (c) 2006 The Thomson Corp
 File 40:Enviroline(R) 1975-2006/Aug
 File 41:Pollution Abstracts 1966-2006/Aug
 (c) 2006 CSA.
 File 45:EMCare 2006/Oct W1
 (c) 2006 Elsevier B.V.
 File 50:CAB Abstracts 1972-2006/Sep
 (c) 2006 CAB International
 File 65:Inside Conferences 1993-2006/Oct 06
 (c) 2006 BLDSC all rts. reserv.
 File 71:ELSEVIER BIOBASE 1994-2006/Oct W1
 (c) 2006 Elsevier B.V.
 File 73:EMBASE 1974-2006/Oct 06
 (c) 2006 Elsevier B.V.
 File 94:JICST-EPlus 1985-2006/Jul W1
 (c)2006 Japan Science and Tech Corp(JST)
 File 98:General Sci Abs 1984-2006/Oct
 (c) 2006 The HW Wilson Co.
 File 103:Energy SciTec 1974-2006/Aug B1
 (c) 2006 Contains copyrighted material
 *File 103: For access restrictions see Help Restrict.
 File 136:BioEngineering Abstracts 1966-2006/Aug
 (c) 2006 CSA.
 File 143:Biol. & Agric. Index 1983-2006/Jul
 (c) 2006 The HW Wilson Co
 File 144:Pascal 1973-2006/Sep W2
 (c) 2006 INIST/CNRS
 File 155:MEDLINE(R) 1950-2006/Oct 09
 (c) format only 2006 Dialog
 File 156:ToxFile 1965-2006/Oct W1
 (c) format only 2006 Dialog
 File 162:Global Health 1983-2006/Aug
 (c) 2006 CAB International
 File 172:EMBASE Alert 2006/Oct 06
 (c) 2006 Elsevier B.V.
 File 305:Analytical Abstracts 1980-2006/Sep W3
 (c) 2006 Royal Soc Chemistry
 *File 305: Alert feature enhanced for multiple files, duplicate
 removal, customized scheduling. See HELP ALERT.
 File 369:New Scientist 1994-2006/Aug W2
 (c) 2006 Reed Business Information Ltd.
 File 370:Science 1996-1999/Jul W3
 (c) 1999 AAAS
 *File 370: This file is closed (no updates). Use File 47 for more current
 information.

File 393:Beilstein Abstracts 2006/Q3

(c) 2006 Beilstein GmbH

File 399:CA SEARCH(R) 1967-2006/UD=14515

(c) 2006 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement.

IPCR/8 classification codes now searchable as IC=. See HELP NEWSIPCR.

File 434:SciSearch(R) Cited Ref Sci 1974-1989/Dec

(c) 2006 The Thomson Corp

Set	Items	Description
-----	-------	-------------

---	-----	-----
-----	-------	-------

?

? ds

Set	Items	Description
S1	390	HEARTWATER AND VACCINE
S2	258	RD S1 (unique items)
S3	206	S2 AND PY<2000
S4	3	S3 AND (MAP2 OR MAP(W)2 OR MAJOR(W)ANTIGENIC(W)PROTEIN)
S5	115	(MAP2 OR MAP(W)2 OR MAJOR(W)ANTIGENIC(W)PROTEIN) AND RUMIN- ANTIUM

S6 42 RD S5 (unique items)

? b biochem

>>> 76 is unauthorized

>>>1 of the specified files is not available

08oct06 15:05:22 User226352 Session D966.4

\$11.59 1.931 DialUnits File5

\$74.80 34 Type(s) in Format 7

\$74.80 34 Types

\$86.39 Estimated cost File5

\$1.67 0.229 DialUnits File6

\$1.67 Estimated cost File6

\$0.45 0.165 DialUnits File10

\$4.35 3 Type(s) in Format 7

\$4.35 3 Types

\$4.80 Estimated cost File10

\$2.93 0.473 DialUnits File24

\$2.50 1 Type(s) in Format 7

\$2.50 1 Types

\$5.43 Estimated cost File24

\$0.38 0.062 DialUnits File28

\$0.38 Estimated cost File28

\$41.11 1.752 DialUnits File34

\$47.74 7 Type(s) in Format 7

\$47.74 7 Types

\$88.85 Estimated cost File34

\$3.08 0.669 DialUnits File50

\$12.00 6 Type(s) in Format 7

\$12.00 6 Types

\$15.08 Estimated cost File50

\$0.32 0.052 DialUnits File64

\$0.32 Estimated cost File64

\$2.02 0.493 DialUnits File65

\$2.02 Estimated cost File65

\$1.30 0.371 DialUnits File94

\$1.30 Estimated cost File94

\$0.51 0.120 DialUnits File98

\$0.51 Estimated cost File98

\$0.55 0.116 DialUnits File99

\$0.55 Estimated cost File99

\$0.29 0.097 DialUnits File143

\$0.29 Estimated cost File143

\$7.70 1.711 DialUnits File144

\$1.65 1 Type(s) in Format 7

\$1.65 1 Types

\$9.35 Estimated cost File144

\$0.56 0.233 DialUnits File203

\$0.56 Estimated cost File203

\$0.36 0.012 DialUnits File235

\$0.36 Estimated cost File235

\$0.25 0.070 DialUnits File266

\$4.20 2 Type(s) in Format 7

\$4.20 2 Types

\$4.45 Estimated cost File266

\$0.11 0.012 DialUnits File306

\$0.11 Estimated cost File306

RESULT 5
 COWIMMDOM
 LOCUS COWIMMDOM 2773 bp DNA linear BCT 06-OCT-1994
 DEFINITION Cowdria ruminantium (clone pF5.2) immunodominant protein, complete cds; ORF, complete cds.
 ACCESSION L07385
 VERSION L07385.1 GI:289922
 KEYWORDS immunodominant protein.
 SOURCE Ehrlichia ruminantium (heartwater rickettsia)
 ORGANISM Ehrlichia ruminantium
 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
 REFERENCE 1 (bases 1 to 2773)
 AUTHORS Mahan,S.M., McGuire,T.C., Semu,S.M., Bowie,M.V., Jongejan,F., Rurangirwa,F.R. and Barbet,A.F.
 TITLE Molecular cloning of a gene encoding the immunogenic 21 kDa protein of Cowdria ruminantium
 JOURNAL Microbiology 140 (Pt 8), 2135-2142 (1994)
 PUBMED 7921263
 COMMENT Original source text: Cowdria ruminantium (library: pUC13 of Suman Mahan) DNA.

FEATURES
 source Location/Qualifiers
 1..2773
 /organism="Ehrlichia ruminantium"
 /mol_type="genomic DNA"
 /db_xref="taxon:779"
 /tissue_lib="pUC13 of Suman Mahan"
 CDS
 1245..1874
 /experiment="experimental evidence, no additional details recorded"
 /codon_start=1
 /transl_table=11
 /product="immunodominant protein"
 /protein_id="AAA50280.1"
 /db_xref="GI:289923"
 /translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQGFQPKLHDSPDV NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ LGNESDKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVVYG QPDNDNQINHSGIMYIVDKKGEYLTHFVPDLKSKEPQVDKLLSLIKQYL"
 sig_peptide
 1245..1301
 /note="putative"
 CDS
 1943..2773
 /note="putative"
 /codon_start=1
 /transl_table=11
 /protein_id="AAA50281.1"
 /db_xref="GI:289924"
 /translation="MKKFLLVLFLLLVMPLPKDSNAEHIHVVGSSTAFFPFAAAIAEEFG RFSDYGTPIIESVSGSMGFSMFQSVENSTPDIAMSSRKIKDAEVELCKSNDVHDIIE IIIGYDGIVIANSNNSNKLDFTKKDLFKALSKYATSEEYTHSIPVNDFKYWSEINNRF PNIDIEVYGPYKNTGTYNILIEEIMQDSCMNHKNFIEVYPDLKKRQHACSMIRNDGKY IEVAANENIIQKIAKNNAAFGIFSFSLIQNQDKIHGNKIAGVEPTYETISSGKYIL S"
 sig_peptide
 1943..2005
 /note="putative"

ORIGIN

Query Match 100.0%; Score 618; DB 15; Length 2773;
 Best Local Similarity 100.0%; Pred. No. 4e-183;
 Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTGGGA 60
 |||
 Db 1257 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTGGGA 1316
 Qy 61 TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT 120
 |||

AUTHORS Mahan,S.M., McGuire,T.C., Semu,S.M., Bowie,M.V., Jongejan,F.,
Rurangirwa,F.R. and Barbet,A.F.
TITLE Molecular cloning of a gene encoding the immunogenic 21 kDa protein
of Cowdria ruminantium
JOURNAL Microbiology 140 (Pt 8), 2135-2142 (1994)
PUBMED 7921263
COMMENT Original source text: Cowdria ruminantium (library: pUC13 of Suman
Mahan) DNA.

FEATURES Location/Qualifiers
source 1..2773
/organism="Ehrlichia ruminantium"
/mol_type="genomic DNA"
/db_xref="taxon:779"
/tissue_lib="pUC13 of Suman Mahan"
CDS 1245..1874
/experiment="experimental evidence, no additional details
recorded"
/codon_start=1
/transl_table=11
/product="immunodominant protein"
/protein_id="AAA50280.1"
/db_xref="GI:289923"
/translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQIFQPKLHDSPDV
NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ
LGNESDKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVVYG
QPDNDNQINHSGIMYIVDKKGEYLTHFVPDLKSKEPQVDKLLSLIKQYL"
sig_peptide 1245..1301
/note="putative"
CDS 1943..2773
/note="putative"
/codon_start=1
/transl_table=11
/protein_id="AAA50281.1"
/db_xref="GI:289924"
/translation="MKKFLLVLFLLLVMPLPKDSNAEHIHVVGSSSTAFPPIAAIAEEFG
RFSYDYGTPPIESVSGSMGFSMFCQSVENSTPDIAMSSRKIKDAEVELCKSNDVHDIIE
IIIGYDGIIVANSNNSNKLDFTKDLFKALSKYATSEEYTHSIPVNDFKYWSEINNRF
PNIDIEVYGPYKNTGTYNILIEEIMQDSCMNHKNFIEVYPDLKKRQHACSMIRNDGKY
IEVAANENIIIQKIAKNNAAFGIFSFSLIQNQDKIHGNKIAGVEPTYETISSGKYIL
S"
sig_peptide 1943..2005
/note="putative"

ORIGIN

Query Match 100.0%; Score 618; DB 15; Length 2773;
Best Local Similarity 100.0%; Pred. No. 4e-183;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA 60
      |||
Db      1257 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA 1316
      |||
Qy      61 TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT 120
      |||
Db      1317 TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT 1376
      |||
Qy      121 AATATATCGAACAAAGCGGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT 180
      |||
Db      1377 AATATATCGAACAAAGCGGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT 1436
      |||
Qy      181 ACGATATCTAGTAAAGACTTCCTTGAAAAACATATGTTAGTCCTTTTTGGGTTTTCTTCT 240
      |||
Db      1437 ACGATATCTAGTAAAGACTTCCTTGAAAAACATATGTTAGTCCTTTTTGGGTTTTCTTCT 1496
      |||
Qy      241 TGTAAAACTATTTGCCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC 300
      |||
Db      1497 TGTAAAACTATTTGCCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC 1556

```

```

Qy      301 AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA 360
      |||
Db      1557 AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA 1616
Qy      361 GAAACACTAAAAGAGTTTACAAAAATTTTGACTCACGGATTCAAATGTTAACAGGAAAC 420
      |||
Db      1617 GAAACACTAAAAGAGTTTACAAAAATTTTGACTCACGGATTCAAATGTTAACAGGAAAC 1676
Qy      421 ATTGAAGCTATTAATCAAATAGTACAAGGTACAAAGTATATGTAGGTCAGCCAGACAAT 480
      |||
Db      1677 ATTGAAGCTATTAATCAAATAGTACAAGGTACAAAGTATATGTAGGTCAGCCAGACAAT 1736
Qy      481 GATAACCAAATTAACCATTTCTGGAATAATGTATATTGTAGACAAGAAAGGAGAATATTTA 540
      |||
Db      1737 GATAACCAAATTAACCATTTCTGGAATAATGTATATTGTAGACAAGAAAGGAGAATATTTA 1796
Qy      541 ACACATTTTGTACCAGATTTAAAGTCAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA 600
      |||
Db      1797 ACACATTTTGTACCAGATTTAAAGTCAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA 1856
Qy      601 ATTAAGCAGTATCTTTAA 618
      |||
Db      1857 ATTAAGCAGTATCTTTAA 1874

```

RESULT 6

AF117728

LOCUS AF117728 630 bp DNA linear BCT 26-JUL-2000

DEFINITION Cowdria ruminantium isolate Palm River major antigenic protein 2 gene, complete cds.

ACCESSION AF117728

VERSION AF117728.1 GI:5163240

KEYWORDS

SOURCE Ehrlichia ruminantium (heartwater rickettsia)

ORGANISM Ehrlichia ruminantium

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.

REFERENCE 1 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.

TITLE Potential value of major antigenic protein 2 for serological diagnosis of heartwater and related ehrlichial infections

JOURNAL Clin. Diagn. Lab. Immunol. 6 (2), 209-215 (1999)

PUBMED 10066656

REFERENCE 2 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.

TITLE Direct Submission

JOURNAL Submitted (05-JAN-1999) Pathobiology, University of Florida, 2015 SW 16th Avenue, Building 1017, Room V2-162, Gainesville, FL 32610, USA

FEATURES

source

Location/Qualifiers

1. .630

/organism="Ehrlichia ruminantium"

/mol_type="genomic DNA"

/isolate="Palm River"

/db_xref="taxon:779"

CDS

1. .630

/codon_start=1

/transl_table=11

/product="major antigenic protein 2"

/protein_id="AAD40617.1"

/db_xref="GI:5163241"

/translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQGFQPKLHDSPOV

NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ

LGNEADKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVYVG

QPDNDNQINHSGIMYIVDKKGEYLAHFVPDLKSKEPQVDKLLSLIKQYL"

ORIGIN

NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ
 LGNESDKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVYVG
 QPDNDNQINHSGIMYIVDKKGEYLTHTFVPLKSKPEQVDKLLSLIKQYL"

ORIGIN

Query Match 100.0%; Score 618; DB 15; Length 630;
 Best Local Similarity 100.0%; Pred. No. 5.3e-183;
 Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA	60
Db	13	ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA	72
Qy	61	TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT	120
Db	73	TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT	132
Qy	121	AATATATCGAACAAAGCGGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT	180
Db	133	AATATATCGAACAAAGCGGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT	192
Qy	181	ACGATATCTAGTAAAGACTTCCTTGGAACCATATGTTAGTCCTTTTTGGGTTTTCTTCT	240
Db	193	ACGATATCTAGTAAAGACTTCCTTGGAACCATATGTTAGTCCTTTTTGGGTTTTCTTCT	252
Qy	241	TGTAAAACTATTTGCCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC	300
Db	253	TGTAAAACTATTTGCCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC	312
Qy	301	AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA	360
Db	313	AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA	372
Qy	361	GAAACACTAAAAGAGTTTCAAAAAATTTGACTCACGGATTCAAATGTTAACAGGAAAC	420
Db	373	GAAACACTAAAAGAGTTTCAAAAAATTTGACTCACGGATTCAAATGTTAACAGGAAAC	432
Qy	421	ATTGAAGCTATTAATCAAATAGTACAAGGGTACAAAGTATATGTAGGTCAGCCAGACAAT	480
Db	433	ATTGAAGCTATTAATCAAATAGTACAAGGGTACAAAGTATATGTAGGTCAGCCAGACAAT	492
Qy	481	GATAACCAAATTAACCATCTGGAATAATGTATATTGTAGACAAGAAAGGAGAATATTTA	540
Db	493	GATAACCAAATTAACCATCTGGAATAATGTATATTGTAGACAAGAAAGGAGAATATTTA	552
Qy	541	ACACATTTTGTACCAGATTTAAAGTCAAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA	600
Db	553	ACACATTTTGTACCAGATTTAAAGTCAAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA	612
Qy	601	ATTAAGCAGTATCTTTAA	618
Db	613	ATTAAGCAGTATCTTTAA	630

RESULT 5

COWIMMDOM

LOCUS COWIMMDOM 2773 bp DNA linear BCT 06-OCT-1994

DEFINITION Cowdria ruminantium (clone pF5.2) immunodominant protein, complete cds; ORF, complete cds.

ACCESSION L07385

VERSION L07385.1 GI:289922

KEYWORDS immunodominant protein.

SOURCE Ehrlichia ruminantium (heartwater rickettsia)

ORGANISM Ehrlichia ruminantium

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 Anaplasmataceae; Ehrlichia.

REFERENCE 1 (bases 1 to 2773)

RESULT 4
 AF117727
 LOCUS AF117727 630 bp DNA linear BCT 26-JUL-2000
 DEFINITION Cowdria ruminantium isolate Highway major antigenic protein 2 gene, complete cds.
 ACCESSION AF117727
 VERSION AF117727.1 GI:5163238
 KEYWORDS
 SOURCE Ehrlichia ruminantium (heartwater rickettsia)
 ORGANISM Ehrlichia ruminantium
 Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
 REFERENCE 1 (bases 1 to 630)
 AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.
 TITLE Potential value of major antigenic protein 2 for serological diagnosis of heartwater and related ehrlichial infections
 JOURNAL Clin. Diagn. Lab. Immunol. 6 (2), 209-215 (1999)
 PUBMED 10066656
 REFERENCE 2 (bases 1 to 630)
 AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.
 TITLE Direct Submission
 JOURNAL Submitted (05-JAN-1999) Pathobiology, University of Florida, 2015 SW 16th Avenue, Building 1017, Room V2-162, Gainesville, FL 32610, USA

FEATURES
 source Location/Qualifiers
 1. .630
 /organism="Ehrlichia ruminantium"
 /mol_type="genomic DNA"
 /isolate="Highway"
 /db_xref="taxon:779"
 CDS
 1. .630
 /codon_start=1
 /transl_table=11
 /product="major antigenic protein 2"
 /protein_id="AAD40616.1"
 /db_xref="GI:5163239"
 /translation="MEHIMKAIKFI LNLCLLFAAIFLGYSYITKQGFQPKLHDSPDV NISNKADINTSFSLINQDGITISSKDFLGKHMVLFGFSSCKTICPMELGLASTILDQ LGNESDKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTG NIEAINQIVQGYKVYVG QPDNDNQINHSGIMYIVDKKGEYLT HFPDLKSKEPQVDKLLSLIKQYL"

ORIGIN

Alignment Scores:

Pred. No.:	4.19e-124	Length:	630
Score:	1054.00	Matches:	205
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	15	Gaps:	0

US-10-722-077-26 (1-205) x AF117727 (1-630)

Qy	1	MetLysAlaIleLysPheIleLeuAsnLeuCysLeuLeuPheAlaAlaIlePheLeuGly	20
Db	13	ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTGGGA	72
Qy	21	TyrSerTyrIleThrLysGlnGlyIlePheGlnProLysLeuHisAspSerProAspVal	40
Db	73	TATTCTTACATAACAAACAAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT	132
Qy	41	AsnIleSerAsnLysAlaAspIleAsnThrSerPheSerLeuIleAsnGlnAspGlyIle	60
Db	133	AATATATCGAACAAAGCGGATATAAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT	192
Qy	61	ThrIleSerSerLysAspPheLeuGlyLysHisMetLeuValLeuPheGlyPheSerSer	80
Db	193	ACGATATCTAGTAAAGACTTCCTTGAAAAACATATGTTAGTCCTTTTTGGGTTTTCTTCT	252

```

Qy      81 CysLysThrIleCysProMetGluLeuGlyLeuAlaSerThrIleLeuAspGlnLeuGly 100
      |||
Db      253 TGTAAAACTATTTGCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC 312

Qy      101 AsnGluSerAspLysLeuGlnValValPheIleThrIleAspProThrLysAspThrVal 120
      |||
Db      313 AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA 372

Qy      121 GluThrLeuLysGluPheHisLysAsnPheAspSerArgIleGlnMetLeuThrGlyAsn 140
      |||
Db      373 GAAACACTAAAAGAGTTTCACAAAAATTTTGACTCACGGATTCAAATGTTAACAGGAAAC 432

Qy      141 IleGluAlaIleAsnGlnIleValGlnGlyTyrLysValTyrValGlyGlnProAspAsn 160
      |||
Db      433 ATTGAAGCTATTAATCAAATAGTACAAGGGTACAAAGTATATGTAGGTCAGCCAGACAAAT 492

Qy      161 AspAsnGlnIleAsnHisSerGlyIleMetTyrIleValAspLysLysGlyGluTyrLeu 180
      |||
Db      493 GATAACCAAATTAACCATTTCTGGAATAATGTATATTGTAGACAAGAAAGGAGAATATTTA 552

Qy      181 ThrHisPheValProAspLeuLysSerLysGluProGlnValAspLysLeuLeuSerLeu 200
      |||
Db      553 ACACATTTTGTACCAGATTTAAAGTCAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA 612

Qy      201 IleLysGlnTyrLeu 205
      |||
Db      613 ATTAAGCAGTATCTT 627

```

RESULT 5

COWIMMDOM

LOCUS COWIMMDOM 2773 bp DNA linear BCT 06-OCT-1994

DEFINITION Cowdria ruminantium (clone pF5.2) immunodominant protein, complete cds; ORF, complete cds.

ACCESSION L07385

VERSION L07385.1 GI:289922

KEYWORDS immunodominant protein.

SOURCE Ehrlichia ruminantium (heartwater rickettsia)

ORGANISM Ehrlichia ruminantium
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehrlichia.

REFERENCE 1 (bases 1 to 2773)

AUTHORS Mahan, S.M., McGuire, T.C., Semu, S.M., Bowie, M.V., Jongejan, F.,
Rurangirwa, F.R. and Barbet, A.F.TITLE Molecular cloning of a gene encoding the immunogenic 21 kDa protein
of Cowdria ruminantium

JOURNAL Microbiology 140 (Pt 8), 2135-2142 (1994)

PUBMED 7921263

COMMENT Original source text: Cowdria ruminantium (library: pUC13 of Suman
Mahan) DNA.

FEATURES

source

Location/Qualifiers

1. .2773

/organism="Ehrlichia ruminantium"

/mol_type="genomic DNA"

/db_xref="taxon:779"

/tissue_lib="pUC13 of Suman Mahan"

CDS

1245. .1874

/experiment="experimental evidence, no additional details
recorded"

/codon_start=1

/transl_table=11

/product="immunodominant protein"

/protein_id="AAA50280.1"

/db_xref="GI:289923"

/translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQGFQPKLHDSPDV
NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ
LGNESDKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVYVG"

sig_peptide QPDNDNQINHSIGIMYIVDKKGEYLTHFVPDLKSKEPQVDKLLSLIKQYL"
 1245..1301
 /note="putative"
 CDS 1943..2773
 /note="putative"
 /codon_start=1
 /transl_table=11
 /protein_id="AAA50281.1"
 /db_xref="GI:289924"
 /translation="MKKFLLVLFLLLVMPLPKDSNAEHIHVVGSSSTAFPFIAAIAEEFG
 RFSYDGTPIIESVSGSMGFSMFCQSVENSTPDIAMSSSRKIKDAEVELCKSNVDHDIIE
 IIGYDGIVIANSNNSNKLDFTKDLFKALSKYATSEYTHSIPVNDFKYWSEINNRF
 PNIDIEVYGPYKNTGTYNILIEEIMQDSCMNHKNFIEVYPDLKKRQHACSMIRNDGKY
 IEVAANENIIQKIAKNNAAFGIFSFSFLIQNQDKIHGNKIAGVEPTYETISSGKYIL
 S"
 sig_peptide 1943..2005
 /note="putative"

ORIGIN

Alignment Scores:

Pred. No.:	2.31e-123	Length:	2773
Score:	1054.00	Matches:	205
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	15	Gaps:	0

US-10-722-077-26 (1-205) x COWIMMDOM (1-2773)

Qy	1	MetLysAlaIleLysPheIleLeuAsnLeuCysLeuLeuPheAlaAlaIlePheLeuGly	20
Db	1257	ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA	1316
Qy	21	TyrSerTyrIleThrLysGlnGlyIlePheGlnProLysLeuHisAspSerProAspVal	40
Db	1317	TATTCTTACATAACAAACAAGGTATATTCCAACCAAAATTACACGACTCTCCTGATGTT	1376
Qy	41	AsnIleSerAsnLysAlaAspIleAsnThrSerPheSerLeuIleAsnGlnAspGlyIle	60
Db	1377	AATATATCGAACAAAGCGGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATT	1436
Qy	61	ThrIleSerSerLysAspPheLeuGlyLysHisMetLeuValLeuPheGlyPheSerSer	80
Db	1437	ACGATATCTAGTAAAGACTTCCTTGGAACATATGTTAGTCCTTTTTGGGTTTTCTTCT	1496
Qy	81	CysLysThrIleCysProMetGluLeuGlyLeuAlaSerThrIleLeuAspGlnLeuGly	100
Db	1497	TGTAAACTATTTGCCCATGGAAGTGGTATAGCATCCACAATTCTAGATCAACTTGGC	1556
Qy	101	AsnGluSerAspLysLeuGlnValValPheIleThrIleAspProThrLysAspThrVal	120
Db	1557	AACGAATCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA	1616
Qy	121	GluThrLeuLysGluPheHisLysAsnPheAspSerArgIleGlnMetLeuThrGlyAsn	140
Db	1617	GAAACACTAAAAGAGTTTCACAAAAATTTTGACTCACGGATTCAAATGTAAACAGGAAAC	1676
Qy	141	IleGluAlaIleAsnGlnIleValGlnGlyTyrLysValTyrValGlyGlnProAspAsn	160
Db	1677	ATTGAAGCTATTAATCAAATAGTACAAGGTACAAAGTATATGTAGGTCAGCCAGACAAAT	1736
Qy	161	AspAsnGlnIleAsnHisSerGlyIleMetTyrIleValAspLysLysGlyGluTyrLeu	180
Db	1737	GATAACCAAAATTAACCATCTGGAATAATGTATATTGTAGACAAGAAAGGAGAAATATTTA	1796
Qy	181	ThrHisPheValProAspLeuLysSerLysGluProGlnValAspLysLeuLeuSerLeu	200

Db 1797 ACACATTTTGTACCAGATTTAAAGTCAAAAGAGCCTCAAGTGGATAAAATTACTTTCTTTA 1856
 Qy 201 ILeLysGlnTyrLeu 205
 |||||
 Db 1857 ATTAAGCAGTATCTT 1871

RESULT 6

AF117728

LOCUS AF117728 630 bp DNA linear BCT 26-JUL-2000

DEFINITION Cowdria ruminantium isolate Palm River major antigenic protein 2 gene, complete cds.

ACCESSION AF117728

VERSION AF117728.1 GI:5163240

KEYWORDS

SOURCE Ehrlichia ruminantium (heartwater rickettsia)

ORGANISM Ehrlichia ruminantium

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.

REFERENCE 1 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.

TITLE Potential value of major antigenic protein 2 for serological diagnosis of heartwater and related ehrlichial infections

JOURNAL Clin. Diagn. Lab. Immunol. 6 (2), 209-215 (1999)

PUBMED 10066656

REFERENCE 2 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.

TITLE Direct Submission

JOURNAL Submitted (05-JAN-1999) Pathobiology, University of Florida, 2015 SW 16th Avenue, Building 1017, Room V2-162, Gainesville, FL 32610, USA

FEATURES

source

Location/Qualifiers

1..630

/organism="Ehrlichia ruminantium"

/mol_type="genomic DNA"

/isolate="Palm River"

/db_xref="taxon:779"

CDS

1..630

/codon_start=1

/transl_table=11

/product="major antigenic protein 2"

/protein_id="AAD40617.1"

/db_xref="GI:5163241"

/translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQGIFQPKLHDSPOV

NISNKADINTSFSLINQDGITISSKDFLGKHLVLFGFSSCKTICPMELGLASTILDQ

LGNEADKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVYVG

QPDNDNQINHSIGIMYIVDKKGEYLAHFVDPDLKSKEPQVDKLLSLIKQYL"

ORIGIN

Alignment Scores:

Pred. No.:	4.36e-123	Length:	630
Score:	1046.00	Matches:	203
Percent Similarity:	99.5%	Conservative:	1
Best Local Similarity:	99.0%	Mismatches:	1
Query Match:	99.2%	Indels:	0
DB:	15	Gaps:	0

US-10-722-077-26 (1-205) x AF117728 (1-630)

Qy 1 MetLysAlaIleLysPheIleLeuAsnLeuCysLeuLeuPheAlaAlaIlePheLeuGly 20
 |||||
 Db 13 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA 72
 Qy 21 TyrSerTyrIleThrLysGlnGlyIlePheGlnProLysLeuHisAspSerProAspVal 40
 |||||
 Db 73 TATTCTTACATAACAAAACAAGGTATATTCCAACCAAAGTTACACGACTCTCCTGATGTT 132
 Qy 41 AsnIleSerAsnLysAlaAspIleAsnThrSerPheSerLeuIleAsnGlnAspGlyIle 60

```

Db      133 |||||AATATATCGAACAAAGCGGATATAAACTAGCTTTAGCTTAATTAATCAGGATGGTATC 192
Qy      61 ThrIleSerSerLysAspPheLeuGlyLysHisMetLeuValLeuPheGlyPheSerSer 80
Db      193 |||||ACGATATCTAGTAAAGACTTCCTTGAAAAACATATGTTAGTCCTTTTGGGTTTTCTTCT 252
Qy      81 CysLysThrIleCysProMetGluLeuGlyLeuAlaSerThrIleLeuAspGlnLeuGly 100
Db      253 |||||TGTAAGAACTATTTGCCCATGGAACTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC 312
Qy      101 AsnGluSerAspLysLeuGlnValValPheIleThrIleAspProThrLysAspThrVal 120
Db      313 |||||AACGAAGCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA 372
Qy      121 GluThrLeuLysGluPheHisLysAsnPheAspSerArgIleGlnMetLeuThrGlyAsn 140
Db      373 |||||GAAACACTAAAAGAGTTTCACAAAAATTTTGACTCACGGATTCAAATGTAAACAGGAAAC 432
Qy      141 IleGluAlaIleAsnGlnIleValGlnGlyTyrLysValTyrValGlyGlnProAspAsn 160
Db      433 |||||ATTGAAGCTATTAATCAAATAGTACAAGGGTATAAAGTATATGTAGGTCAACCAGACAAT 492
Qy      161 AspAsnGlnIleAsnHisSerGlyIleMetTyrIleValAspLysLysGlyGluTyrLeu 180
Db      493 |||||GATAACCAAATTAACCATCTGGAATAATGTATATTGTAGATAAGAAAGGAGAATATTTA 552
Qy      181 ThrHisPheValProAspLeuLysSerLysGluProGlnValAspLysLeuLeuSerLeu 200
Db      553 |||||GCACATTTTGTACCAGATTTAAAGTCAAAGAGCCTCAAGTAGATAAAATTACTTTCTTTA 612
Qy      201 IleLysGlnTyrLeu 205
Db      613 |||||ATTAAGCAGTATCTT 627

```

RESULT 7

AF117729

LOCUS AF117729 630 bp DNA linear BCT 26-JUL-2000
 DEFINITION Cowdria ruminantium isolate Um Banein major antigenic protein 2 gene, complete cds.

ACCESSION AF117729

VERSION AF117729.1 GI:5163242

KEYWORDS

SOURCE Ehrlichia ruminantium (heartwater rickettsia)

ORGANISM Ehrlichia ruminantium

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.

REFERENCE 1 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.
 TITLE Potential value of major antigenic protein 2 for serological diagnosis of heartwater and related ehrlichial infections

JOURNAL Clin. Diagn. Lab. Immunol. 6 (2), 209-215 (1999)

PUBMED 10066656

REFERENCE 2 (bases 1 to 630)

AUTHORS Bowie,M.V., Reddy,G.R., Semu,S.M., Mahan,S.M. and Barbet,A.F.
 TITLE Direct Submission

JOURNAL Submitted (05-JAN-1999) Pathobiology, University of Florida, 2015 SW 16th Avenue, Building 1017, Room V2-162, Gainesville, FL 32610, USA

FEATURES

source

Location/Qualifiers

1. .630

/organism="Ehrlichia ruminantium"

/mol_type="genomic DNA"

/isolate="Um Banein"

/db_xref="taxon:779"

CDS

1. .630

/codon_start=1

```

/transl_table=11
/product="major antigenic protein 2"
/protein_id="AAD40618.1"
/db_xref="GI:5163243"
/translation="MEHIMKAIKFILNLCLLFAAIFLGYSYITKQGIFQPKLHDSPOV
NISNKADINTSFSLINQDGITISSKDFLGKHMVLVFGFSSCKTICPMELGLASTILDQ
LGNEADKLQVVFITIDPTKDTVETLKEFHKNFDSRIQMLTGNIEAINQIVQGYKVYVG
QPDNDNQINHSGIMYIVDKKGEYLAHFVPDLKSKEPQVDKLLSLIKQYL"

```

ORIGIN

Alignment Scores:

Pred. No.:	4.36e-123	Length:	630
Score:	1046.00	Matches:	203
Percent Similarity:	99.5%	Conservative:	1
Best Local Similarity:	99.0%	Mismatches:	1
Query Match:	99.2%	Indels:	0
DB:	15	Gaps:	0

US-10-722-077-26 (1-205) x AF117729 (1-630)

```

Qy      1 MetLysAlaIleLysPheIleLeuAsnLeuCysLeuLeuPheAlaAlaIlePheLeuGly 20
      |||
Db      13 ATGAAGGCTATCAAGTTTATACTTAATCTATGTTTACTATTTGCAGCAATTTTTTTGGGA 72

Qy      21 TyrSerTyrIleThrLysGlnGlyIlePheGlnProLysLeuHisAspSerProAspVal 40
      |||
Db      73 TATTCTTACATAACAAACAAGGTATATTCCAACCAAAGTTACACGACTCTCCTGATGTT 132

Qy      41 AsnIleSerAsnLysAlaAspIleAsnThrSerPheSerLeuIleAsnGlnAspGlyIle 60
      |||
Db      133 AATATATCGAACAAAGCTGATATAAATACTAGCTTTAGCTTAATTAATCAGGATGGTATC 192

Qy      61 ThrIleSerSerLysAspPheLeuGlyLysHisMetLeuValLeuPheGlyPheSerSer 80
      |||
Db      193 ACGATATCTAGTAAAGACTTCCTTGGAACCATATGTTAGTCCTTTTTGGGTTTTCTTCT 252

Qy      81 CysLysThrIleCysProMetGluLeuGlyLeuAlaSerThrIleLeuAspGlnLeuGly 100
      |||
Db      253 TGTAACAACTATTTGCCCCATGGAAGTAGGGTTAGCATCCACAATTCTAGATCAACTTGGC 312

Qy      101 AsnGluSerAspLysLeuGlnValValPheIleThrIleAspProThrLysAspThrVal 120
      |||
Db      313 AACGAAGCTGACAAGTTACAAGTAGTCTTTATAACTATTGATCCAACAAAAGATACTGTA 372

Qy      121 GluThrLeuLysGluPheHisLysAsnPheAspSerArgIleGlnMetLeuThrGlyAsn 140
      |||
Db      373 GAAACACTAAAAGAGTTTCACAAAAATTTGACTCACGGATTCAAATGTTAACAGGAAAC 432

Qy      141 IleGluAlaIleAsnGlnIleValGlnGlyTyrLysValTyrValGlyGlnProAspAsn 160
      |||
Db      433 ATTGAAGCTATTAATCAATAGTACAAGGGTATAAAGTATATGTAGGTCAACCAGACAAT 492

Qy      161 AspAsnGlnIleAsnHisSerGlyIleMetTyrIleValAspLysLysGlyGluTyrLeu 180
      |||
Db      493 GATAACCAAATTAACCACTTCTGGAATAATGTATATTGTAGATAAGAAAGGAGAATATTTA 552

Qy      181 ThrHisPheValProAspLeuLysSerLysGluProGlnValAspLysLeuLeuSerLeu 200
      |||
Db      553 GCACATTTTGTACCAGATTTAAAGTCAAAGAGCCTCAAGTAGATAAATTACTTTCTTTA 612

Qy      201 IleLysGlnTyrLeu 205
      |||
Db      613 ATTAAGCAGTATCTT 627

```